

FIG. 1A.

2/10

GCCTACGACACGGTCCGCTGGGAGTTCGGCACCTGCCAGCCGCTGTCAGACGAGAAGGAC
721-----+-----+-----+-----+-----+-----+-----+-----+ 780
A Y D T V R W E F G T C Q P L S D E K D -
CTGACCCAGCTCTTCATGTTCCGCCGGAATGCCTTACCCTGCTGGCCATGATGGACTAC
781-----+-----+-----+-----+-----+-----+-----+-----+ 840
L T Q L F M F A R N A F T V L A M M D Y -
CCCTACCCCACTGACTTCCTGGGTCCCTCCCTGCCAACCCCGTCAAGGTGGGCTGTGAT
841-----+-----+-----+-----+-----+-----+-----+-----+ 900
P Y P T D F L G P L P A N P V K V G C D -
CGGCTGCTGAGTGAGGCCAGAGGATCACGGGGCTGCGAGCACTGGCAGGGCTGGTCTAC
901-----+-----+-----+-----+-----+-----+-----+-----+ 960
R L L S E A Q R I T G L R A L A G L V Y -
AACGCCTCGGGCTCCGAGCACTGCTACGACATCTACCGGCTCTACCACAGCTGTGCTGAC
961-----+-----+-----+-----+-----+-----+-----+-----+ 1020
N A S G S E H C Y D I Y R L Y H S C A D -
CCCACTGGCTGCGGCACCGGCCCGACGCCAGGGCCTGGGACTACCAGGCCTGCACCGAG
1021-----+-----+-----+-----+-----+-----+-----+-----+ 1080
P T G C G T G P D A R A W D Y Q A C T E -
ATCAACCTGACCTTCGCCAGCAACAATGTGACCGATATGTTCCCGACCTGCCCTTCACT
1081-----+-----+-----+-----+-----+-----+-----+-----+ 1140
I N L T F A S N N V T D M F P D L P F T -
GACGAGCTCCGCCAGCGGTACTGCCTGGACACCTGGGGCGTGTGGCCCCGGCCCCGACTGG
1141-----+-----+-----+-----+-----+-----+-----+-----+ 1200
D E L R Q R Y C L D T W G V W P R P D W -
CTGCTGACCAGCTTCTGGGGGGTGATCTCAGAGCCGCCAGCAACATCATCTTCTCCAAC
1201-----+-----+-----+-----+-----+-----+-----+-----+ 1260
L L T S F W G G D L R A A S N I I F S N -
GGGAACCTGGACCCCTGGGCAGGGGGCGGGATTCCGAGGAACCTGAGTGCCTCAGTCATC
1261-----+-----+-----+-----+-----+-----+-----+-----+ 1320
G N L D P W A G G G I R R N L S A S V I -
GCCGTCACCATCCAGGGGGGAGCGCACCACTCGACCTCAGAGCCTCCCACCCAGAAGAT
1321-----+-----+-----+-----+-----+-----+-----+-----+ 1380
A V T I Q G G A H H L D L R A S H P E D -
CCTGCTTCCGTGGTTGAGGCGCGGAAGCTGGAGGCCACCATCATCGGCGAGTGGGTAAAG
1381-----+-----+-----+-----+-----+-----+-----+-----+ 1440
P A S V V E A R K L E A T I I G E W V K -
GCAGCCAGGCGTGAGCAGCAGCCAGCTCTGCGTGGGGGGCCAGACTCAGCCTCTGAGCA
1441-----+-----+-----+-----+-----+-----+-----+-----+ 1500
A A R R E Q Q P A L R G G P R L S L -
CAGGACTGGAGGGGTCTCAAGGCTCCTCATGGAGTGGGGGCTTCACTCAAGCAGCTGGCG
1501-----+-----+-----+-----+-----+-----+-----+-----+ 1560

FIG. 1B.

209020" 4E T2900T

3/10

GCAGAGGGAAGGGGCTGAATAAACGCCTGGAGGCCTGGCAAAAAAAAAAAAAAAAAAAAAA
1561-----+-----+-----+-----+-----+-----+ 1620

AAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1621-----+-----+-----+----- 1653

FIG. 1C.

20030207 "4E" 22007

4/10

```

-----
Query: 22012
Scores for sequence family classification (score includes all domains):
Model      Description      Score      E-value      N
-----
abhydrolase alpha/beta hydrolase fold      31.8      1.6e-05      1
Peptidase_S9 Prolyl oligopeptidase family      8.4      0.25      1

Parsed for domains:
Model      Domain      seq-f      seq-t      hmm-f      hmm-t      score      E-value
-----
Peptidase_S9 1/1      158      167      .      72      81      .      8.4      0.25
abhydrolase 1/1      100      360      .      1      233      {}      31.8      1.6e-05

Alignments of top-scoring domains:
Peptidase_S9: domain 1 of 1, from 158 to 167: score 8.4, E = 0.25
      *->ifGgSnGGIL<-*
      +fGgS+GG+L
22012 158 AFGGSYGGML 167

abhydrolase: domain 1 of 1, from 100 to 360: score 31.8, E = 1.6e-05
      *->frviaIDlrGfGeSsrp.....sdladyrfddlaedleal
      + ++ + trttG+S p + ++++++++ + + +d+ae l al
22012 100 ALLVFAEHRYYGKSL-PfgaqstqrghteLLTVEQALADFAELLRAL 145

      ldalglakp.vilvGhSmGgalaayaakyPeervkalvlvstp...ap
      ++ lg + ++i++G+S+GG+l+a++++kyP+ +v+++ + s+p a
22012 146 RRDLGAQDApAIAFGGSYGGMLSAYLRMKYPH-LVAGALAASAPvlavAG 194

      aglssrlfprlgnleglllanffnrlsrsveallgralkqffllgrpfv
      g s+ +f++ ++ ++ ++ +++++ +ea++++ + +fl g +
22012 195 LGDSNQFFRDVTADFEQSPCKTQ---GVREAFRQIKD--LFLQGAY--- 236

      dflkqaedwlsslarp.getdggdglly...avalgkllqwdrs.alkd
      d ++++++++ l++++ t+ ++ ++ + + + + +d+ ++l+
22012 237 DTVRWEFGTCQPLSDEKDLTQLFMFARNAftvLAMMDYPYPTDFLgPLPA 286

      ..ikvPtIviwgddDplvplkaseklsalfpna.evsviddagHla...
      +++kv + + +++ l a l + +++ ++i +H +++
22012 287 npVKVGCDRLLEAQRITGLRALAGLVYNASGSeHCYDIYRLYHSCadpt 336

      .....llekpeevaeli.kfl<-*
      + +++++ ++++++e+ f+
22012 337 gcgtgpdarAWDYQACTEINITFA 360
  
```

//

FIG. 2.

200920 "4E139001"

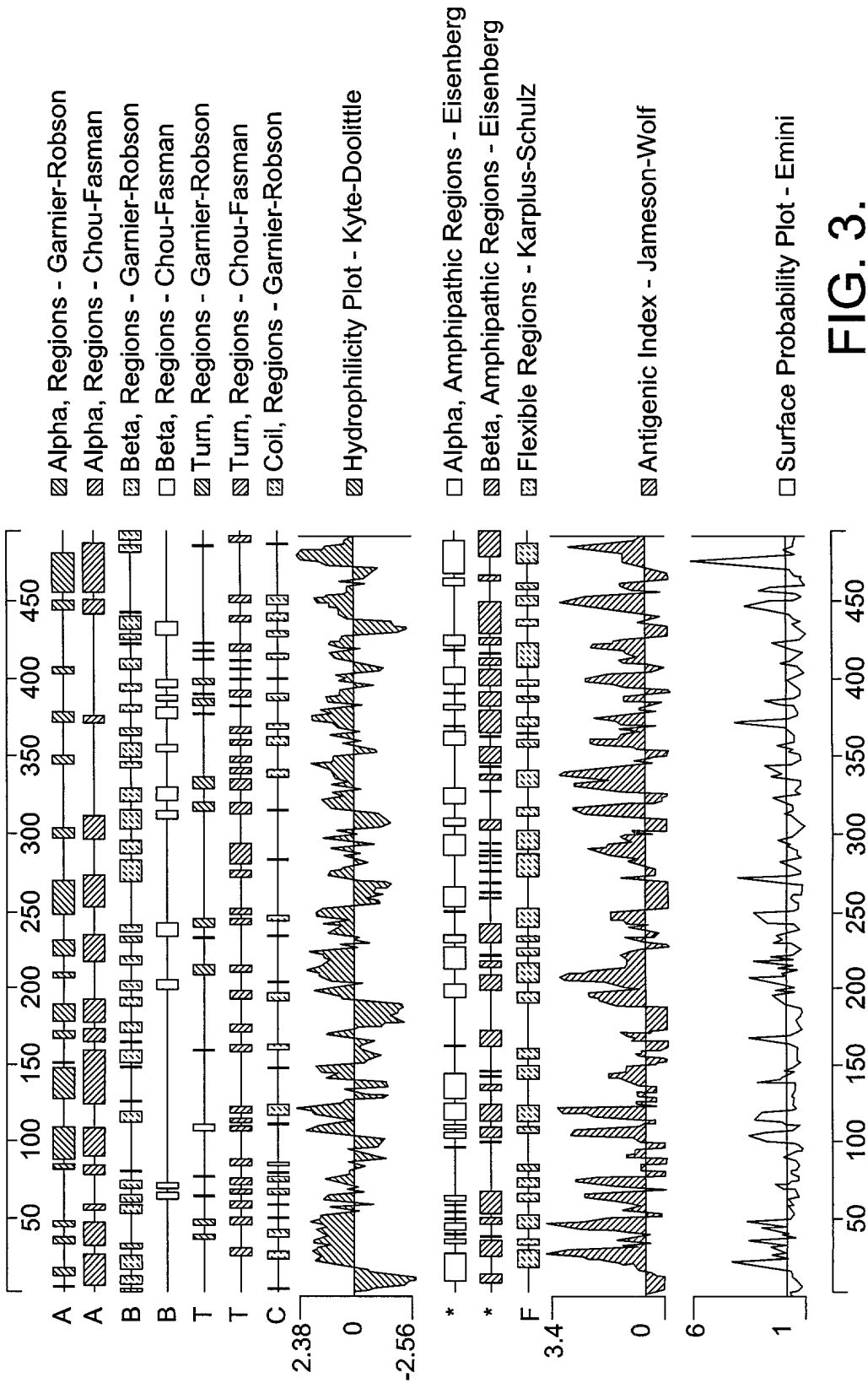
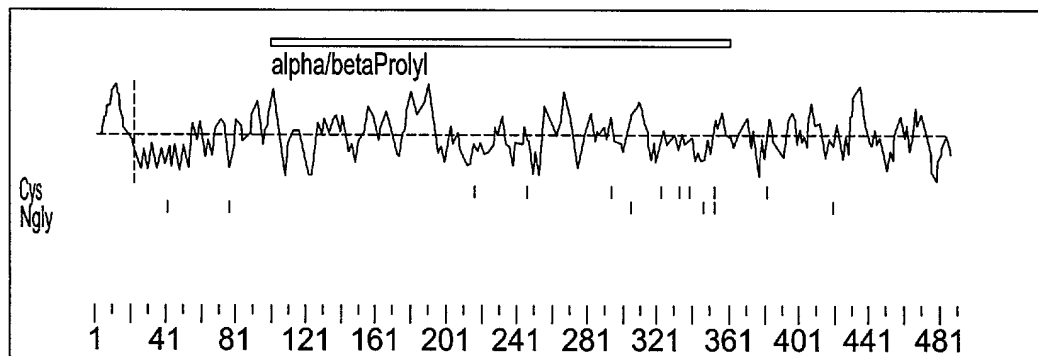


FIG. 3.

6/10

Analysis of 22012 (492 aa)



>22012
MGSAPWAPVLLALGLRGLQAGARRAPDPGFQERFFQQRLDHFNFRFGNKTFPQRFLVS
DRFWVRGEGPIFFYTGNEGDVWAFANNSGFVAELAAERGALLVFAEHRYYGKSLPFGAQS
TQRGHTELLTVEQALADFAELLRALRRDLGAQDAPATAFGGSYGGMLSAYLRMKYPHLVA
GALAASAPVLAVAGLGDSNQFFRDVTADFEQSPKCTQGVREAFRQIKDLFLQGAYDVR
WEFGTCQPLSDEKDLTQLFMFARNAFTVLAMMDYPYPTDFLGPLPANPYKVGC DRLLSEA
QRITGLRALAGLVYNASGSEHCYDIYRLYHSCADPTGCGTGP DARAWDYQACTEINLTFA
SNNVTDMFPDLPTDELRRQRYCLDTWGVWPRPDWLLTSFWGGDLRAASNIFSNGLDPW
AGGGIRRNLSASVIAVTIQGGAHLDLRASHPEDPASVVEARKLEATTIGEWVKAARREQ
QPALRGGPRLSL

FIG. 4.

7/10

Prosites Pattern Matches for 22012

Prosites version: Release 12.2 of February 1995

>PS00001/PDOC00001/ASN_GLYCOSYLATION N-glycosylation site.

Query:	50	NKTF	53
Query:	86	NNSG	89
Query:	315	NASG	318
Query:	356	NLTF	359
Query:	363	NVTD	366
Query:	428	NLSA	431

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query:	60	SDR	62
Query:	121	TQR	123
Query:	213	SPK	215
Query:	238	TVR	240

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query:	75	TGNE	78
Query:	317	SGSE	320
Query:	331	SCAD	334
Query:	340	TGPD	343
Query:	450	SHPE	453
Query:	457	SVVE	460

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query:	18	GLQAGA	23
Query:	117	GAQSTQ	122
Query:	160	GGSYGG	165
Query:	181	GALAAS	186
Query:	194	GLGDSN	199
Query:	219	GVREAF	224
Query:	234	GAYDTV	239
Query:	311	GLVYNA	316
Query:	318	GSEHCY	323
Query:	424	GIRRNL	429

>PS00029/PDOC00029/LEUCINE_ZIPPER Leucine zipper pattern.

Query:	128	LLTVEQALADFAELLRALRRDL	149
--------	-----	------------------------	-----

FIG. 5.

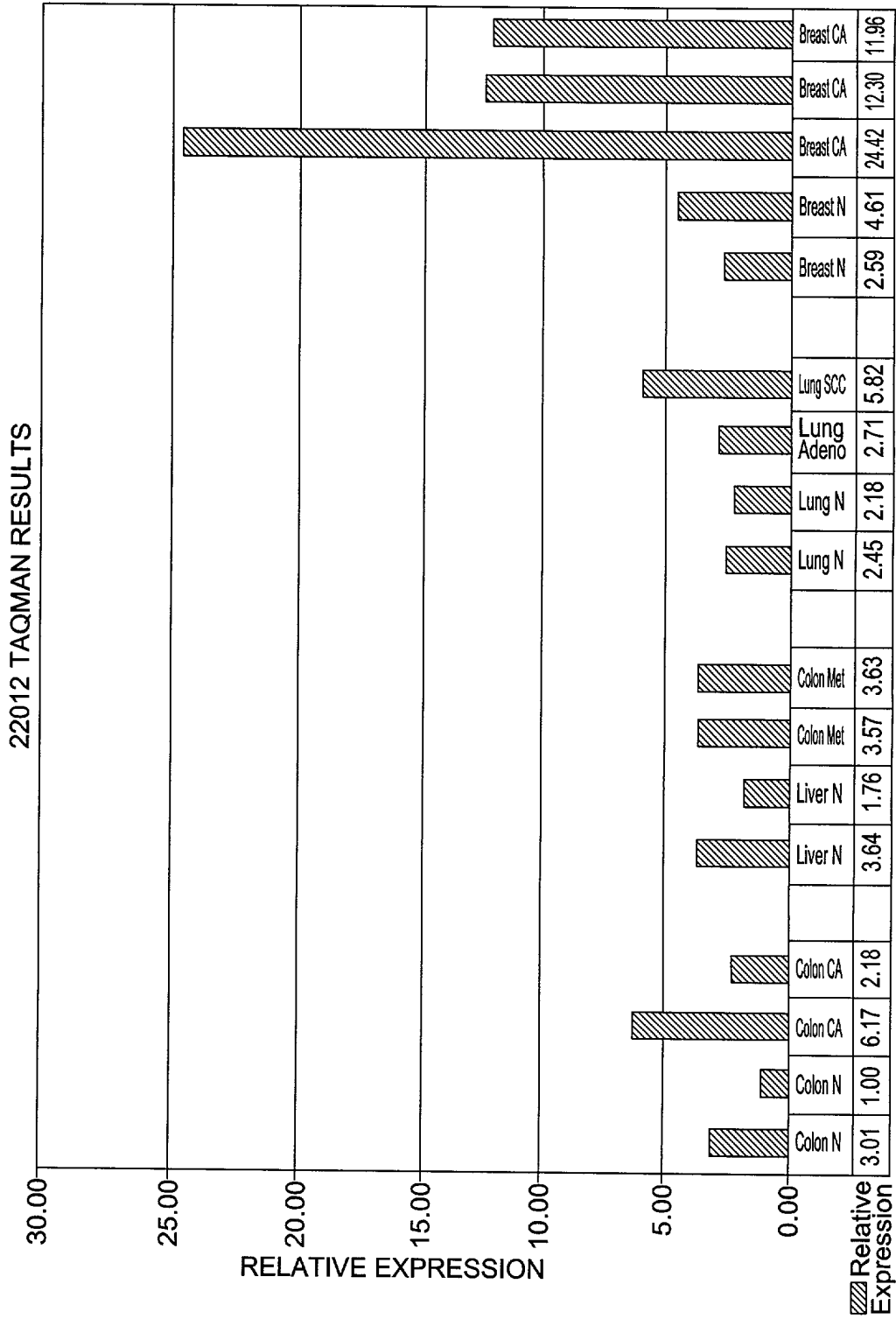


FIG. 6.

Gene 22012 Expression in Normal Human Tissues

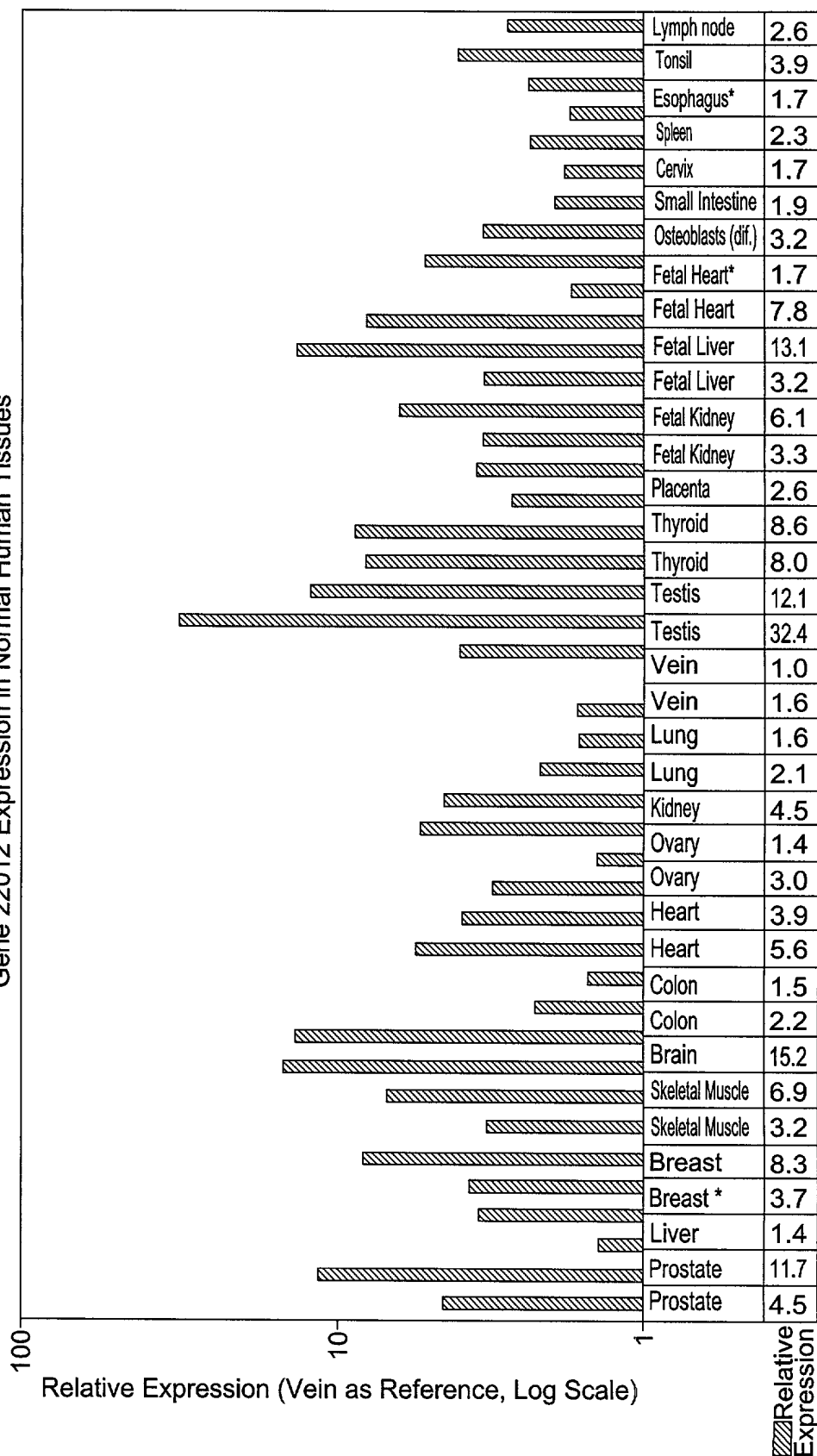


FIG. 7.

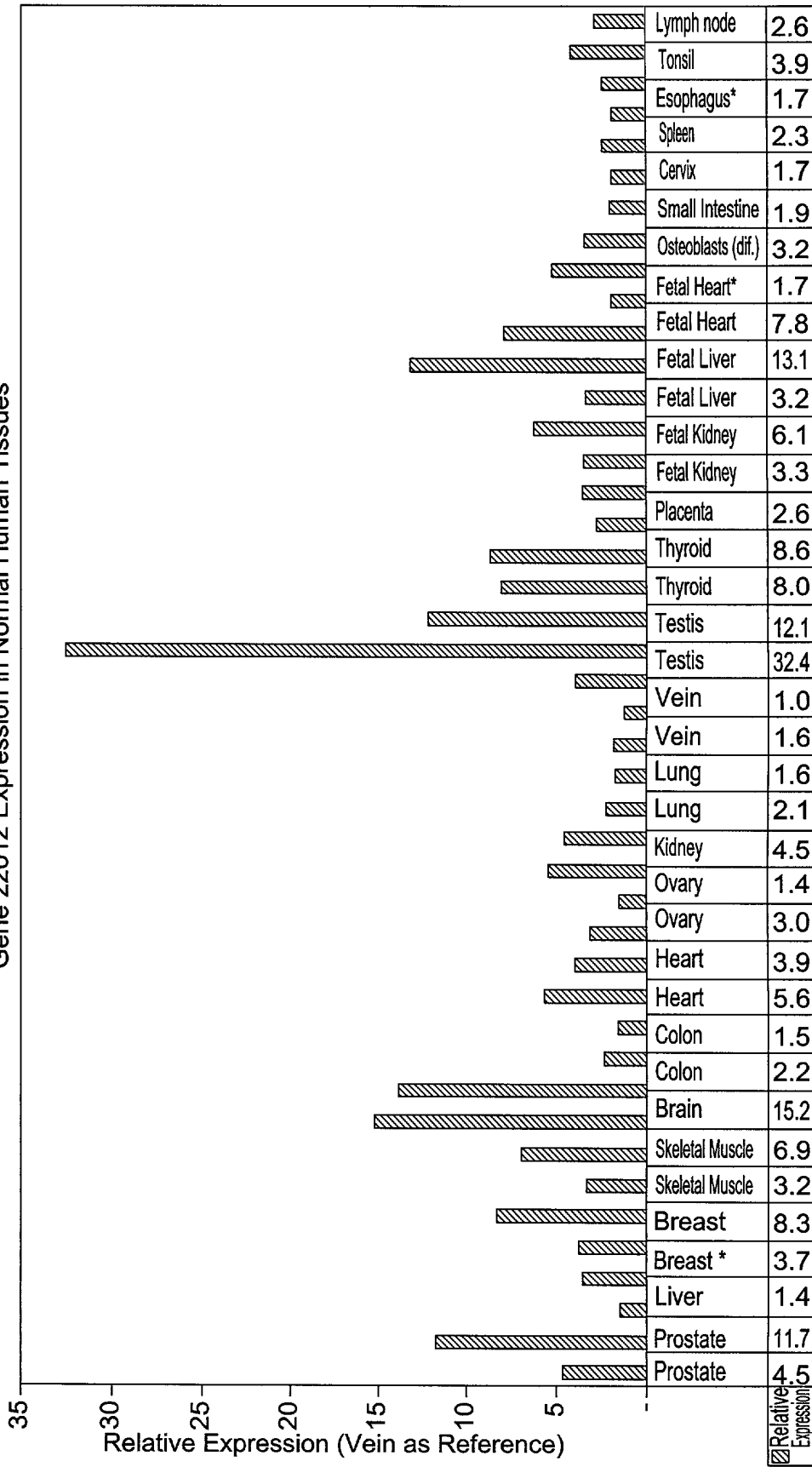
Tissue Type

Relative Expression (Vein as Reference, Log Scale)

Relative Expression

10/10

Gene 22012 Expression in Normal Human Tissues



Tissue Type

FIG. 8.